```
          10                  30                  50
CGATCGCCCAGCACCAAGTCCGCTTCCAGGCTTTCGGTTTCTTTGCCTCCATCTTGGGTG

          70                  90                 110
CGCCTTCCCGGCGTCTAGGGGAGCGAAGGCTGAGGTGGCAGCGGCAGGAGAGTCCGGCCG

         130                 150                 170
CGACAGGACGAACTCCCCCACTGGAAAGGATTCTGAAAGAAATGAAGTCAGCCCTCAGAA

         190                 210                 230
ATGAAGTTGACTGCCTGCTGGCTTTCTGTTGACTGGCCCGGAGCTGTACTGCAAGACCCT

         250                 270                 290
TGTGAGCTTCCCTAGTCTAAGAGTAGGATGTCTGCTGAAGTCATCCATCAGGTTGAAGAA
                             M   S   A   E   V   I   H   Q   V   E   E
         310                 330                 350
GCACTTGATACAGATGAGAAGGAGATGCTGCTCTTTTTGTGCCGGGATGTTGCTATAGAT
A   L   D   T   D   E   K   E   M   L   L   F   L   C   R   D   V   A   I   D

         370                 390                 410
GTGGTTCCACCTAATGTCAGGGACCTTCTGGATATTTTACGGGAAAGAGGTAAGCTGTCT
V   V   P   P   N   V   R   D   L   L   D   I   L   R   E   R   G   K   L   S

         430                 450                 470
GTCGGGGACTTGGCTGAACTGCTCTACAGAGTGAGGCGATTTGACCTGCTCAAACGTATC
V   G   D   L   A   E   L   L   Y   R   V   R   R   F   D   L   L   K   R   I

         490                 510                 530
TTGAAGATGGACAGAAAAGCTGTGGAGACCCACCTGCTCAGGAACCCTCACCTTGTTTCG
L   K   M   D   R   K   A   V   E   T   H   L   L   R   N   P   H   L   V   S

         550                 570                 590
GACTATAGAGTGCTGATGGCAGAGATTGGTGAGGATTTGGATAAATCTGATGTGTCCTCA
D   Y   R   V   L   M   A   E   I   G   E   D   L   D   K   S   D   V   S   S

         610                 630                 650
TTAATTTTCCTCATGAAGGATTACATGGGCCGAGGCAAGATAAGCAAGGAGAAGAGTTTC
L   I   F   L   M   K   D   Y   M   G   R   G   K   I   S   K   E   K   S   F

         670                 690                 710
TTGGACCTTGTGGTTGAGTTGGAGAAACTAAATCTGGTTGCCCCAGATCAACTGGATTTA
L   D   L   V   V   E   L   E   K   L   N   L   V   A   P   D   Q   L   D   L

         730                 750                 770
TTAGAAAAATGCCTAAAGAACATCCACAGAATAGACCTGAAGACAAAAATCCAGAAGTAC
L   E   K   C   L   K   N   I   H   R   I   D   L   K   T   K   I   Q   K   Y

         790                 810                 830
AAGCAGTCTGTTCAAGGAGCAGGGACAAGTTACAGGAATGTTCTCCAAGCAGCAATCCAA
K   Q   S   V   Q   G   A   G   T   S   Y   R   N   V   L   Q   A   A   I   Q

         850                 870                 890
AAGAGTCTCAAGGATCCTTCAAATAACTTCAGGCTCCATAATGGGAGAAGTAAAGAACAA
K   S   L   K   D   P   S   N   N   F   R   L   H   N   G   R   S   K   E   Q

         910                 930                 950
AGACTTAAGGAACAGCTTGGCGCTCAACAAGAACCAGTGAAGAAATCCATTCAGGAATCA
R   L   K   E   Q   L   G   A   Q   Q   E   P   V   K   K   S   I   Q   E   S

         970                 990                1010
GAAGCTTTTTTGCCTCAGAGCATACCTGAAGAGAGATACAAGATGAAGAGCAAGCCCCTA
E   A   F   L   P   Q   S   I   P   E   E   R   Y   K   M   K   S   K   P   L
        1030                1050                1070
```

FIG.1A

```
GGAATCTGCCTGATAATCGATTGCATTGGCAATGAGACAGAGCTTCTTCGAGACACCTTC
G  I  C  L  I  I  D  C  I  G  N  E  T  E  L  L  R  D  T  F

      1090                1110                1130
ACTTCCCTGGGCTATGAAGTCCAGAAATTCTTGCATCTCAGTATGCATGGTATATCCCAG
T  S  L  G  Y  E  V  Q  K  F  L  H  L  S  M  H  G  I  S  Q

      1150                1170                1190
ATTCTTGGCCAATTTGCCTGTATGCCCGAGCACCGAGACTACGACAGCTTTGTGTGTGTC
I  L  G  Q  F  A  C  M  P  E  H  R  D  Y  D  S  F  V  C  V

      1210                1230                1250
CTGGTGAGCCGAGGAGGCTCCCAGAGTGTGTATGGTGTGGATCAGACTCACTCAGGGCTC
L  V  S  R  G  G  S  Q  S  V  Y  G  V  D  Q  T  H  S  G  L

      1270                1290                1310
CCCCTGCATCACATCAGGAGGATGTTCATGGGAGATTCATGCCCTTATCTAGCAGGGAAG
P  L  H  H  I  R  R  M  F  M  G  D  S  C  P  Y  L  A  G  K

      1330                1350                1370
CCAAAGATGTTTTTTATTCAGAACTATGTGGTGTCAGAGGGCCAGCTGGAGGACAGCAGC
P  K  M  F  F  I  Q  N  Y  V  V  S  E  G  Q  L  E  D  S  S

      1390                1410                1430
CTCTTGGAGGTGGATGGGCCAGCGATGAAGAATGTGGAATTCAAGGCTCAGAAGCGAGGG
L  L  E  V  D  G  P  A  M  K  N  V  E  F  K  A  Q  K  R  G

      1450                1470                1490
CTGTGCACAGTTCACCGAGAAGCTGACTTCTTCTGGAGCCTGTGTACTGCGGACATGTCC
L  C  T  V  H  R  E  A  D  F  F  W  S  L  C  T  A  D  M  S

      1510                1530                1550
CTGCTGGAGCAGTCTCACAGCTCACCGTCCCTGTACCTGCAGTGCCTCTCCCAGAAACTG
L  L  E  Q  S  H  S  S  P  S  L  Y  L  Q  C  L  S  Q  K  L

      1570                1590                1610
AGACAAGAAAGAAAACGCCCACTCCTGGATCTTCACATTGAACTCAATGGCTACATGTAT
R  Q  E  R  K  R  P  L  L  D  L  H  I  E  L  N  G  Y  M  Y

      1630                1650                1670
GATTGGAACAGCAGAGTTTCTGCCAAGGAGAAATATTATGTCTGGCTGCAGCACACTCTG
D  W  N  S  R  V  S  A  K  E  K  Y  Y  V  W  L  Q  H  T  L

      1690                1710                1730
AGAAAGAAACTTATCCTCTCCTACACATAAGAAACCAAAAGGCTGGGCGTAGTGGCTCGC
R  K  K  L  I  L  S  Y  T  *

      1750                1770                1790
ACCTGTAATCCCAGCACTTTGGGAGGCCAAGGAGGGCGGATCACTTCAGGTCAGGAGTTC

      1810                1830                1850
GAGACCAGCCTGGCCAACATGGTAAACGCTGTCCCTAGTAAGAGTGCAAAAATTAGCTGG

      1870                1890                1910
GTGTGGGTGTGGGTACCTGTGTTCCCAGTTACTTGGGAGGCTGAGGTGGGAGGATCTTTT

      1930                1950                1970
GAACCCAGGAGTTCAGGGTCATAGCATGCTGTGATTGTGCCTACGAATAGCCACTGCATA

      1990                2010                2030
CCAACCTGGGCAATATAGCAAGATCCCATCTTTTTAAAAAAAAAAAAAAAAAAA
```

FIG. 1B

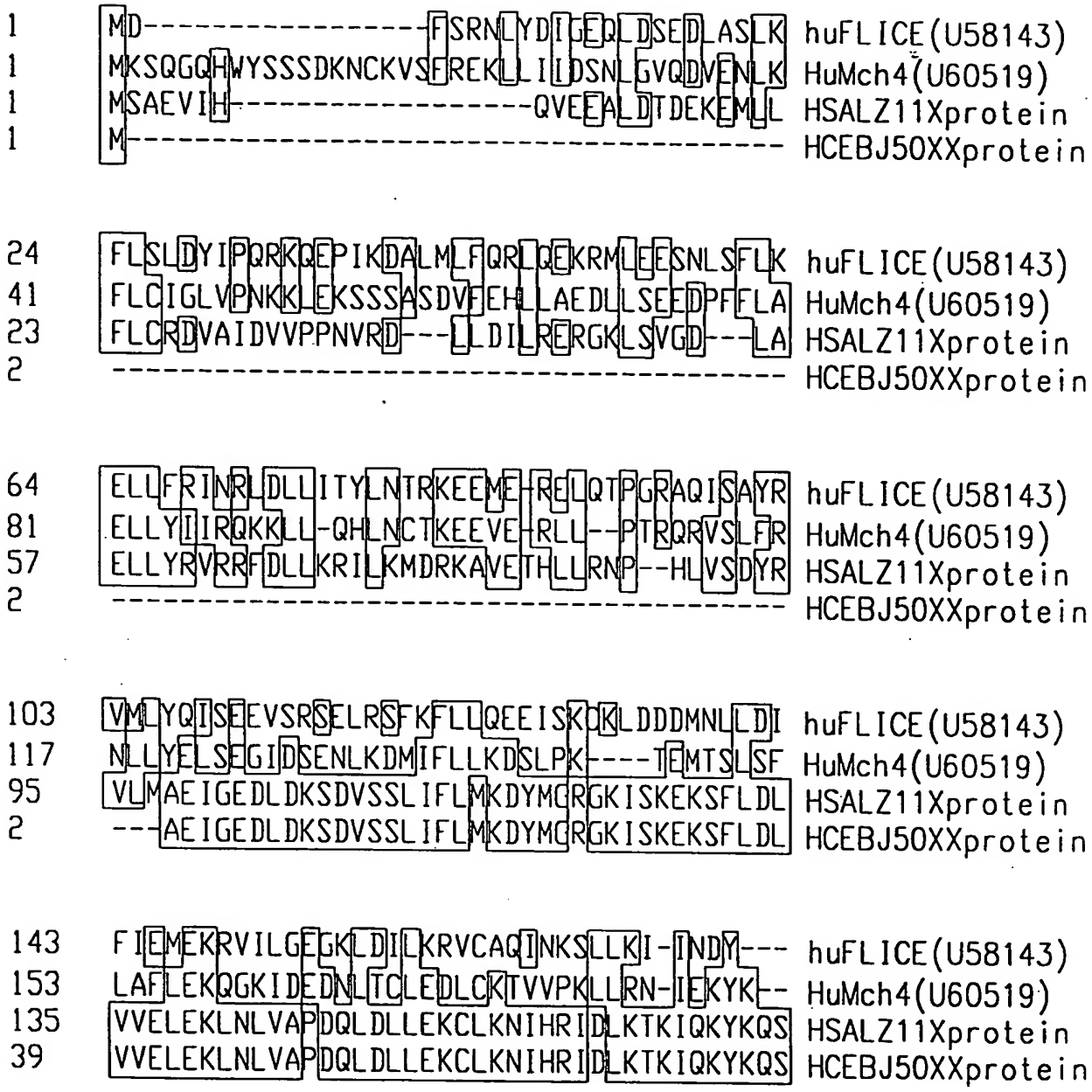

1 MD----------FSRNLYDIGEQLDSEDLASLK huFLICE(U58143)
1 MKSQGQHWYSSSDKNCKVSFREKLLIIDSNLGVQDVENLK HuMch4(U60519)
1 MSAEVIH----------QVEEALDTDEKEMLL HSALZ11Xprotein
1 M---------- HCEBJ50XXprotein
24 FLSLDYIPQRKQEPIKDALMLFQRLQEKRMLEESNLSFLK huFLICE(U58143)
41 FLCIGLVPNKKLEKSSSASDVFEHLLAEDLLSEEDPFFLA HuMch4(U60519)
23 FLCRDVAIDVVPPNVRD---LLDILRERGKLSVGD---LA HSALZ11Xprotein
2 ---------- HCEBJ50XXprotein
64 ELLFRINRLDLLITYLNTRKEEMERELQTPGRAQISAYR huFLICE(U58143)
81 ELLYIIRQKKLL-QHLNCTKEEVERLL--PTRQRVSLFR HuMch4(U60519)
57 ELLYRVRRFDLLKRILKMDRKAVETHLLRNP--HLVSDYR HSALZ11Xprotein
2 ---------- HCEBJ50XXprotein
103 VMLYQISEEVSRSELRSFKFLLQEEISKCKLDDDMNLLDI huFLICE(U58143)
117 NLLYELSEGIDSENLKDMIFLLKDSLPK----TEMTSLSF HuMch4(U60519)
95 VLMAEIGEDLDKSDVSSLIFLMKDYMGRGKISKEKSFLDL HSALZ11Xprotein
2 ---AEIGEDLDKSDVSSLIFLMKDYMGRGKISKEKSFLDL HCEBJ50XXprotein
143 FIEMEKRVILGEGKLDILKRVCAQINKSLLKI-INDY--- huFLICE(U58143)
153 LAFLEKQGKIDEDNLTCLEDLCKTVVPKLLRN-IEKYK-- HuMch4(U60519)
135 VVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQS HSALZ11Xprotein
39 VVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQS HCEBJ50XXprotein

FIG.2A

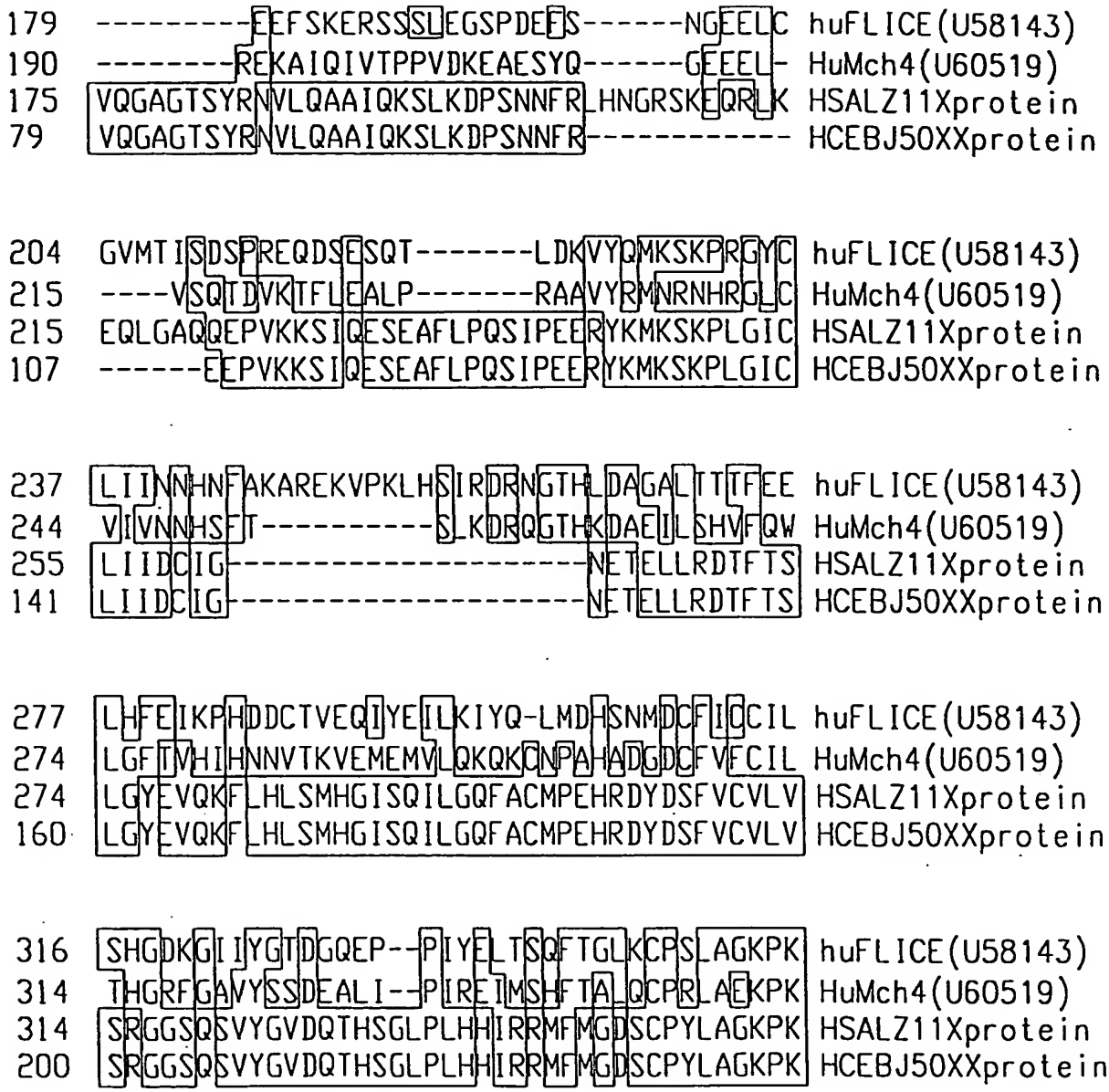

179 ---------EEFSKERSSSLEGSPDEFS------NGEELC huFLICE(U58143)
190 --------REKAIQIVTPPVDKEAESYQ------GEEEL- HuMch4(U60519)
175 VQGAGTSYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLK HSALZ11Xprotein
79 VQGAGTSYRNVLQAAIQKSLKDPSNNFR---------- HCEBJ50XXprotein
204 GVMTISDSPREQDSESQT-------LDKVYQMKSKPRGYC huFLICE(U58143)
215 ----VSQTDVKTFLEALP-------RAAVYRMNRNHRGLC HuMch4(U60519)
215 EQLGAQQEPVKKSIQESEAFLPQSIPEERYKMKSKPLGIC HSALZ11Xprotein
107 ------EEPVKKSIQESEAFLPQSIPEERYKMKSKPLGIC HCEBJ50XXprotein
237 LIINNHNFAKAREKVPKLHSIRDRNGTHLDAGALTTTFEE huFLICE(U58143)
244 VIVNNHSFT----------SLKDRQGTHKDAEILSHVFQW HuMch4(U60519)
255 LIIDCIG----------NETELLRDTFTS HSALZ11Xprotein
141 LIIDCIG----------NETELLRDTFTS HCEBJ50XXprotein
277 LHFEIKPHDDCTVEQIYEILKIYQ-LMDHSNMDCFICCIL huFLICE(U58143)
274 LGFTVHIHNNVTKVEMEMVLQKQKCNPAHADGDCFVFCIL HuMch4(U60519)
274 LGYEVQKFLHLSMHGISQILGQFACMPEHRDYDSFVCVLV HSALZ11Xprotein
160 LGYEVQKFLHLSMHGISQILGQFACMPEHRDYDSFVCVLV HCEBJ50XXprotein
316 SHGDKGIIYGTDGQEP--PIYELTSQFTGLKCPSLAGKPK huFLICE(U58143)
314 THGRFGAVYSSDEALI--PIREIMSHFTALQCPRLAEKPK HuMch4(U60519)
314 SRGGSQSVYGVDQTHSGLPLHHIRRMFMGDSCPYLAGKPK HSALZ11Xprotein
200 SRGGSQSVYGVDQTHSGLPLHHIRRMFMGDSCPYLAGKPK HCEBJ50XXprotein

FIG.2B

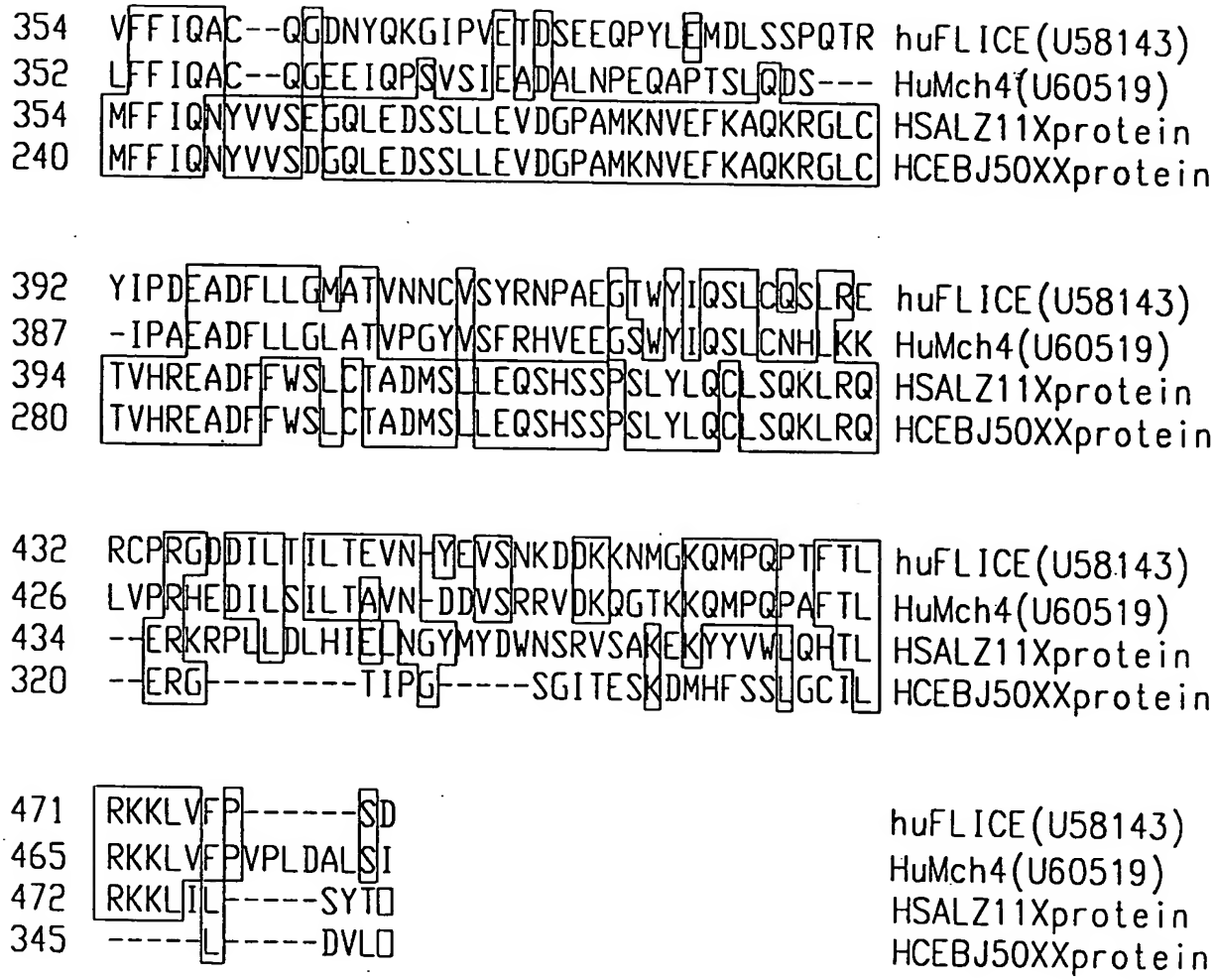
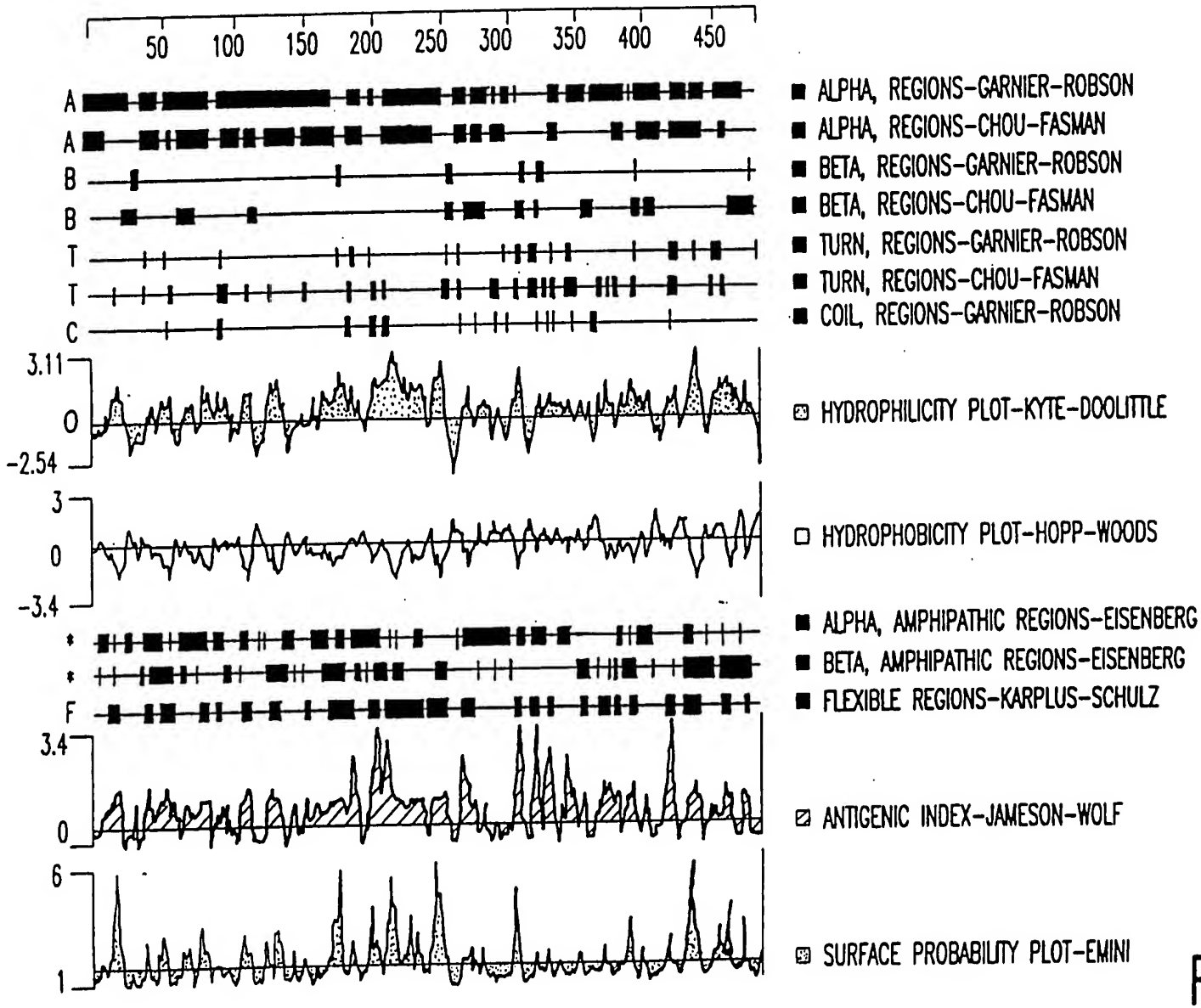

354 VFFIQAC--QGDNYQKGIPVETDSEEQPYLEMDLSSPQTR huFLICE(U58143)
352 LFFIQAC--QGEEIQPSVSIEADALNPEQAPTSLQDS--- HuMch4(U60519)
354 MFFIQNYVVSEGQLEDSSLLEVDGPAMKNVEFKAQKRGLC HSALZ11Xprotein
240 MFFIQNYVVSDGQLEDSSLLEVDGPAMKNVEFKAQKRGLC HCEBJ50XXprotein
392 YIPDEADFLLGMATVNNCVSYRNPAEGTWYIQSLCQSLRE huFLICE(U58143)
387 -IPAEADFLLGLATVPGYVSFRHVEEGSWYIQSLCNHLKK HuMch4(U60519)
394 TVHREADFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQ HSALZ11Xprotein
280 TVHREADFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQ HCEBJ50XXprotein
432 RCPRGDDILTILTEVNHYEVSNKDDKKNMGKQMPQPTFTL huFLICE(U58143)
426 LVPRHEDILSILTAVN-DDVSRRVDKQGTKKQMPQPAFTL HuMch4(U60519)
434 --ERKRPLLDLHIELNGYMYDWNSRVSAKEKYYVWLQHTL HSALZ11Xprotein
320 --ERG-------TIPG-----SGITESKDMHFSSLGCIL HCEBJ50XXprotein
471 RKKLVFP------SD huFLICE(U58143)
465 RKKLVFPVPLDALSI HuMch4(U60519)
472 RKKLIL-----SYT HSALZ11Xprotein
345 -----L-----DVL HCEBJ50XXprotein

FIG.2C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TURN, REGIONS-CHOU-FASMAN
COIL, REGIONS-GARNIER-ROBSON
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0
-3.4
HYDROPHOBICITY PLOT-HOPP-WOODS
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FLEXIBLE REGIONS-KARPLUS-SCHULZ
3.4
0
ANTIGENIC INDEX-JAMESON-WOLF
6
1
SURFACE PROBABILITY PLOT-EMINI

FIG.3

```
        10                  30                  50
GCGAGCTTGCAGCCTCACCGACGAGTCTCAACTAAAAGGGACTCCCGGAGCTAGGGGTGG

        70                  90                  110
GGACTCGGCCTCACACAGTGATTGCCGGCTATTGGACTTTTGTCCAGTGACAGCTGAGAC

        130                 150                 170
AACAAGGACCACGGGAGGAGGTGTAGGAGAGAAGCGCCGCGAACAGGCATCGCCCAGCAC

        190                 210                 230
CAAGTCCGCTTCCAGGCTTTCGGTTTCTTTGCCTCCATCTTGGGTGCGCCTTCCCGGCGT

        250                 270                 290
CTAGGGGAGCGAAGGCTGAGGTGGCAGCGGCAGGAGAGTCCGGCCGCGACAGGACGAGTG

        310                 330                 350
CTGATGGCAGAGATTGGTGAGGATTTGGATAAATCTGATGTGTCCTCATTAATTTTCCTC
   M  A  E  I  G  E  D  L  D  K  S  D  V  S  S  L  I  F  L

        370                 390                 410
ATGAAGGATTACATGGGCCGAGGCAAGATAAGCAAGGAGAAGAGTTTCTTGGACCTTGTG
M  K  D  Y  M  G  R  G  K  I  S  K  E  K  S  F  L  D  L  V

        430                 450                 470
GTTGAGTTGGAGAAACTAAATCTGGTTGCCCCAGATCAACTGGATTTATTAGAAAAATGC
V  E  L  E  K  L  N  L  V  A  P  D  Q  L  D  L  L  E  K  C
        490                 510                 530
```

FIG.4A

```
CTAAAGAACATCCACAGAATAGACCTGAAGACAAAAATCCAGAAGTACAAGCAGTCTGTT
L  K  N  I  H  R  I  D  L  K  T  K  I  Q  K  Y  K  Q  S  V
      550                 570                 590
CAAGGAGCAGGGACAAGTTACAGGAATGTTCTCCAAGCAGCAATCCAAAAGAGTCTCAAG
Q  G  A  G  T  S  Y  R  N  V  L  Q  A  A  I  Q  K  S  L  K
      610                 630                 650
GATCCTTCAAATAACTTCAGGGAAGAACCAGTGAAGAAATCCATTCAGGAATCAGAAGCT
D  P  S  N  N  F  R  E  E  P  V  K  K  S  I  Q  E  S  E  A
      670                 690                 710
TTTTTGCCTCAGAGCATACCTGAAGAGAGATACAAGATGAAGAGCAAGCCCCTAGGAATC
F  L  P  Q  S  I  P  E  E  R  Y  K  M  K  S  K  P  L  G  I
      730                 750                 770
TGCCTGATAATCGATTGCATTGGCAATGAGACAGAGCTTCTTCGAGACACCTTCACTTCC
C  L  I  I  D  C  I  G  N  E  T  E  L  L  R  D  T  F  T  S
      790                 810                 830
CTGGGCTATGAAGTCCAGAAATTCTTGCATCTCAGTATGCATGGTATATCCCAGATTCTT
L  G  Y  E  V  Q  K  F  L  H  L  S  M  H  G  I  S  Q  I  L
      850                 870                 890
GGCCAATTTGCCTGTATGCCCGAGCACCGAGACTACGACAGCTTTGTGTGTGTCCTGGTG
G  Q  F  A  C  M  P  E  H  R  D  Y  D  S  F  V  C  V  L  V
      910                 930                 950
AGCCGAGGAGGCTCCCAGAGTGTGTATGGTGTGGATCAGACTCACTCAGGGCTCCCCCTG
S  R  G  G  S  Q  S  V  Y  G  V  D  Q  T  H  S  G  L  P  L
      970                 990                1010
CATCACATCAGGAGGATGTTCATGGGAGATTCATGCCCTTATCTAGCAGGGAAGCCAAAG
H  H  I  R  R  M  F  M  G  D  S  C  P  Y  L  A  G  K  P  K
     1030                1050                1070
ATGTTTTTTATTCAGAACTATGTGGTGTCAGACGGCCAGCTGGAGGACAGCAGCCTCTTG
M  F  F  I  Q  N  Y  V  V  S  D  G  Q  L  E  D  S  S  L  L
     1090                1110                1130
GAGGTGGATGGGCCAGCGATGAAGAATGTGGAATTCAAGGCTCAGAAGCGAGGGCTGTGC
E  V  D  G  P  A  M  K  N  V  E  F  K  A  Q  K  R  G  L  C
     1150                1170                1190
ACAGTTCACCGAGAAGCTGACTTCTTCTGGAGCCTGTGTACTGCGGACATGTCCCTGCTG
T  V  H  R  E  A  D  F  F  W  S  L  C  T  A  D  M  S  L  L
     1210                1230                1250
GAGCAGTCTCACAGCTCACCGTCCCTGTACCTGCAGTGCCTCTCCCAGAAACTGAGACAA
E  Q  S  H  S  S  P  S  L  Y  L  Q  C  L  S  Q  K  L  R  Q
     1270                1290                1310
GAAAGGGGGACAATTCCCGGAAGTGGAATTACAGAGTCAAAGGACATGCATTTTTCAAGC
E  R  G  T  I  P  G  S  G  I  T  E  S  K  D  M  H  F  S  S
     1330                1350                1370
CTCGGATGCATCTTACTAGATGTCCTATAGGATGGTCATATCAGCTTTATAGGAGAGTAG
L  G  C  I  L  L  D  V  L  *
     1390                1410                1430
CTGTGTCCCTGAATTCTCCCTGACACTGCATGCTCTTATATTTCCTCAAGTTTTGACAAT
     1450                1470                1490
TTGATAGGTGAAAAGTGGTATCTGACTGTTCAGATCTGGAAGGCTTTGTTATATAAACAT
     1510                1530                1550
TTTTTTAATGTTTATTGGCAAGAATACTTTTCTAAGAGAAACATCAGTGAGCTGGTTTCC
     1570                1590                1610
ATTTAAGCTGAATGAAGCCACAATGTACCTCAAGTATAAGATTAACTGGCCTTTTTCAGT
     1630                1650                1670
TGCACTCTAATTACAATTTAGAATGATGTTTCTGAGCCACCTGTCAAATGCATTCTGGGC
```

FIG.4B

1690 1710 1730
TGTACCTCTGCGTACCCCAGGAATAAATCTCATGGCCTTCTTTACCTGGCCTCCTTAGTG

1750 1770 1790
GTGGCCCAGCAGGAAGCGGGGGTTAGAGCAGGAGCCACTCAGCCTTCCAAGATAGATACT

1810 1830 1850
CCATGGGCCGGTGGTATTACTGGCCTTTTGAGCCCATCCCCATTTGCATAGATGATCCAC

1870 1890 1910
GTGGGTTATCATCTGGCTGGTATGTTCCCAGAGTGAAACTCAGCAGCCCCTTGAGGGAGG

1930 1950 1970
GGATGGTGGCCATCAGGCCAGAGTATTGCAAGTTAGTTTGGATCATTTGCTAAGCAGCTT

1990 2010 2030
GTGGTGCCTTCAGAAAGGAACAGTTTCAAAGAACTTTCACATCTGTTGGCTCATTTCGCC

2050 2070 2090
CTAATGACAGTCTTCTCTTTGATATTTGCATGGCATTAAATTTTGCCTTTCTTGTTTTCT

2110 2130 2150
CCAGAAAACGCCCACTCCTGGATCTTCACATTGAACTCAATGGCTACATGTATGATTGGA

2170 2190 2210
ACAGCAGAGTTTCTGCCAAGGAGAAATATTATGTCTGGCTGCAGCACACTCTGAGAAAGA

2230 2250 2270
AACTTATCTCTCCTACACATAAGAAACCAAAAGGCTGGGCGTAGTGGCTCGCACCTGTGA

2290 2310 2330
TCCCAGCACTTTGGGAGGCCGAGGAGGGCGGATCACTTCAGGTCGGGAGTTCGAGACCAG

2350 2370 2390
CCTGGCCAGCATGTGAACGCTGTCCCTAGTAGAAGTGCAAAAATTGGCTGGTGTGGGTGT

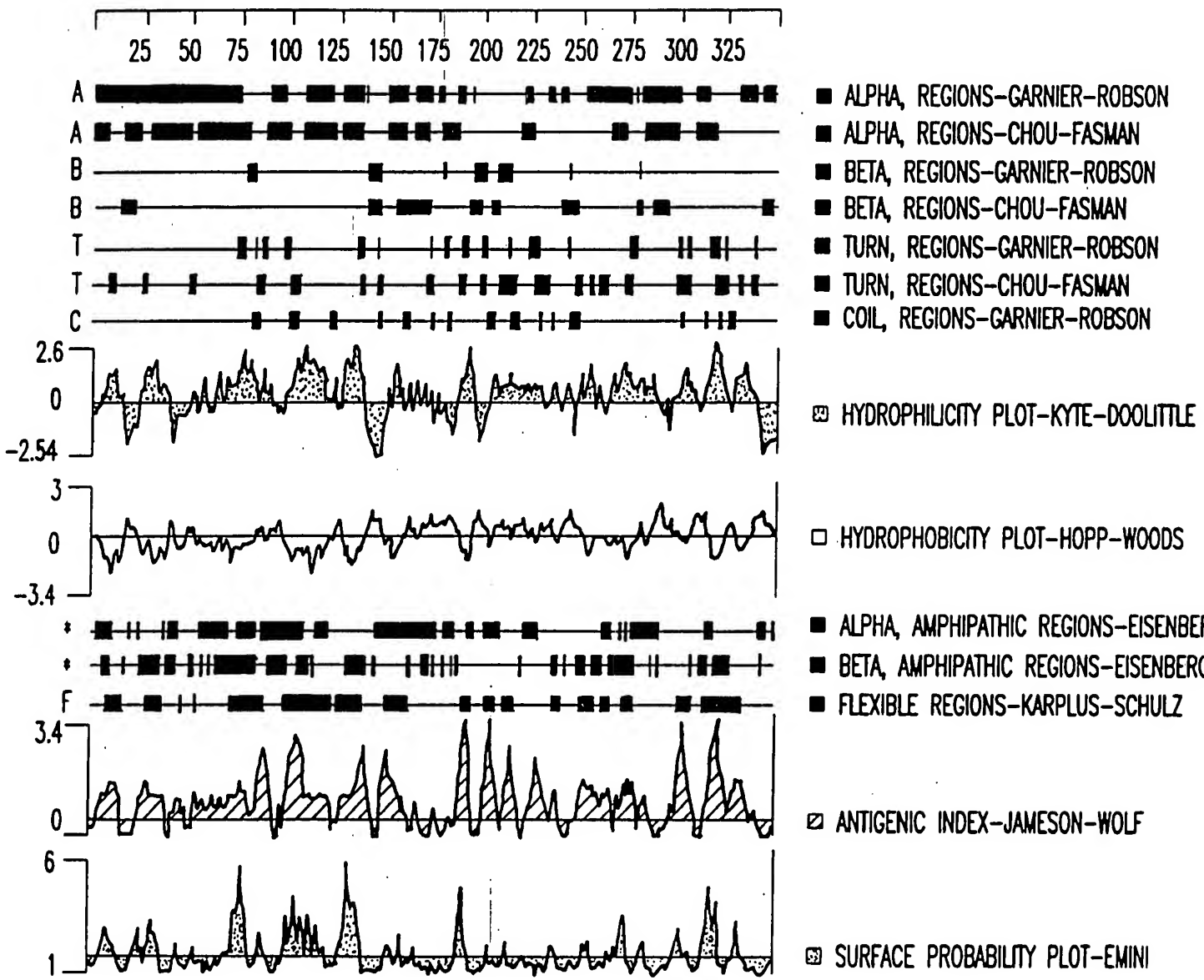
2410 2430 2450
GGGTACCCTGTATTCCCAGTTGCTTGGGGGGCTGAGGTGGGAGGATCTTTTGACCCCAGG

2470 2490 2510
AGTTCAGGGTCATAGCATGCTGTGATTGTGCCTACGAATAGCCACTGCATACCAACCTGG

2530 2550 2570
GCAATATAGCAAGATCCCATCTCTTTAAAAAAAAAAAAAAAAAGGACAGGAACTATCTTAA

2590
AAAAAAAAAAAAAAAA

FIG.4C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BETA, REGIONS-GARNIER-ROBSON
BETA, REGIONS-CHOU-FASMAN
TURN, REGIONS-GARNIER-ROBSON
TURN, REGIONS-CHOU-FASMAN
COIL, REGIONS-GARNIER-ROBSON
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HYDROPHOBICITY PLOT-HOPP-WOODS
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BETA, AMPHIPATHIC REGIONS-EISENBERG
FLEXIBLE REGIONS-KARPLUS-SCHULZ
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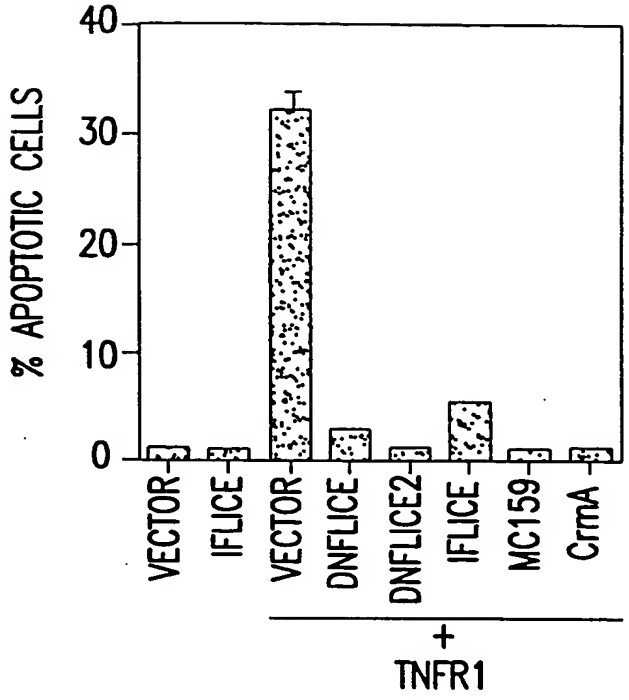
ANTIGENIC INDEX-JAMESON-WOLF
6
1
SURFACE PROBABILITY PLOT-EMINI

FIG.5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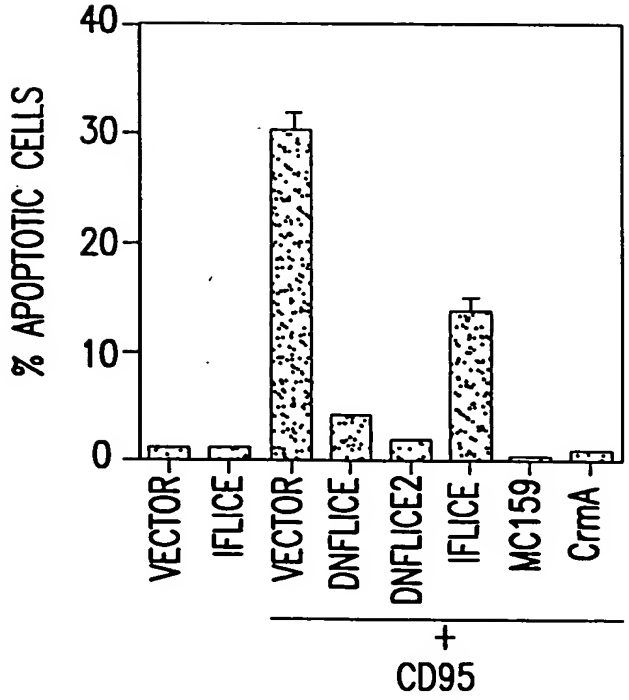
IFLICE
VECTOR
DNFLICE
DNFLICE2
IFLICE
MC159
CrmA
+
TNFR1

FIG.6A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DNFLICE2
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CrmA
+
CD95

FIG.6B